RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/538,343_
Source: _PCT_
Date Processed by STIC: _6/27/05_

ENTERED

Serial Number: _10/538,343_   CRF Edit Date: _6/27/05_
Edited by: _TC_

_____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

_____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

_____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

_✓_ Deleted: _✓_ invalid beginning/end-of-file text ; ___ page numbers

_____ Inserted mandatory headings/numeric identifiers, specifically:

_____

_____ Moved responses to same line as heading/numeric identifier, specifically:

_____

_____ Other:

_____
_____
_____

Revised 09/09/2003

Raw Sequence Listing before editing,
for reference only

PCT

RAW SEQUENCE LISTING   DATE: 06/27/2005
PATENT APPLICATION: US/10/538,343   TIME: 14:48:12

Input Set : **A:\pto.kd.txt**
Output Set: **N:\CRF4\06272005\J538343.raw**

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 3 <110> APPLICANT: Gibson, Keith
 4         Hansen, Lone
 6 <120> TITLE OF INVENTION: Detergent composition
 8 <130> FILE REFERENCE: 10383.204-US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/538,343
C--> 10 <141> CURRENT FILING DATE: 2005-06-10
10 <160> NUMBER OF SEQ ID NOS: 12
12 <170> SOFTWARE: PatentIn version 3.3
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 2322
16 <212> TYPE: DNA
17 <213> ORGANISM: Bacillus sp.
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (1)..(2322)
24 <400> SEQUENCE: 1
25 gca gaa gga aac act cgt gaa gac aat ttt aaa cat tta tta ggt aat      48
26 Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn
27 1               5                   10                  15
29 gac aat gtt aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa      96
30 Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu
31              20                  25                  30
33 gtc gat gga caa atg aca tta gta gat caa cat gga gaa aaa att caa     144
34 Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
35          35                  40                  45
37 tta cgt gga atg agt aca cac gga tta caa tgg ttt cct gar atc ttg     192
38 Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
39      50                  55                  60
41 aat gat aac gca tac aaa gct ctt gct aac gat tgg gaa tca aat atg     240
42 Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met
43 65                  70                  75                  80
45 att cgt cta gct atg tat gtc ggt gaa aat ggc tat gct tca aat cca     288
46 Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro
47                  85                  90                  95
49 gag tta att aaa agc aga gtc att aaa gga ata gat ctt gct att gaa     336
50 Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu
51              100                 105                 110
53 aat gac atg tat gtt att gtt gat tgg cat gta cat gca cct ggt gat     384
54 Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
55          115                 120                 125
57 cct aga gat ccc gtt tac gct gga gca gaa gat ttc ttt aga gat att     432
58 Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile
59      130                 135                 140
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 61 gca gca tta tat cct aac aat cca cac att att tat gag tta gcg aat      480
 62 Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
 63 145                 150           .       155                 160
 65 gag cca agt agt aac aat aat ggt gga gct ggg att cca aat aat gaa      528
 66 Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
 67                 165               170                 175
 69 gaa ggt tgg aat gcg gta aaa gaa tac gct gat cca att gta gaa atg      576
 70 Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
 71             180                 185                 190
 73 tta cgt gat agc ggg aac gca gat gac aat atc atc att gtg ggt agt      624
 74 Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
 75         195                 200                 205
 77 cca aac tgg agt cag cgt cct gac tta gca gct gat aat cca att aat      672
 78 Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asn
 79     210                 215                 220
 81 gat cac cat aca atg tat act gtt cac ttc tac act ggt tca cat gct      720
 82 Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
 83 225                 230                 235                 240
 85 gct tca act gag agc tat ccg cct gaa act cct aac tct gaa aga gga      768
 86 Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
 87                 245                 250                 255
 89 aac gta atg agt aac act cgt tat gcg tta gaa aac gga gta gcg gta      816
 90 Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
 91             260                 265                 270
 93 ttt gcg aca gaa tgg gga aca agt caa gca aat gga gat ggt ggt cct      864
 94 Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro
 95         275                 280                 285
 97 tat ttt gat gaa gca gat gta tgg att gag ttt tta aat gaa aac aac      912
 98 Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
 99     290                 295                 300
101 att agt tgg gct aac tgg tct tta acg aat aaa aat gaa gtg tct ggt      960
102 Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
103 305                 310                 315                 320
105 gca ttt aca cca ttc gag tta ggt aag tct aac gca acc aat ctt gac     1008
106 Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp
107                 325                 330                 335
109 cca ggt cca gat cat gtg tgg gca cca gaa gag tta agt ctt tcg gga     1056
110 Pro Gly Pro Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly
111             340                 345                 350
113 gaa tat gta cgt gct cgt att aaa ggt gtg aac tat gag cca atc gac     1104
114 Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
115         355              .     360                 365
117 cgt aca aaa tac acg aaa gta ctt tgg gac ttt aat gat gga acg aag     1152
118 Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
119     370                 375                 380
121 caa gga ttt gga gtg aat tcg gat tct cca aat aaa gaa ctt att gca     1200
122 Gln Gly Phe Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala
123 385                 390                 395                 400
125 gtt gat aat gaa aac aac act ttg aaa gtt tcg gga tta gat gta agt     1248
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126 Val Asp Asn Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser
127             405                 410                 415
129 aac gat gtt tca gat ggc aac ttc tgg gct aat gct cgt ctt tct gcc    1296
130 Asn Asp Val Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala
131             420                 425                 430
133 gac ggt tgg gga aaa agt gtt gat att tta ggt gct gag aag ctt aca    1344
134 Asp Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr
135             435                 440                 445
137 atg gat gtt att gtt gat gaa cca acg acg gta gct att gcg gcg att    1392
138 Met Asp Val Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile
139     450                 455                 460
141 cca caa agt agt aaa agt gga tgg gca aat cca gag cgt gct gtt cga    1440
142 Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg
143 465                 470                 475                 480
145 gtg aac gcg gaa gat ttt gtt cag caa acg gac ggt aag tat aaa gct    1488
146 Val Asn Ala Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala
147                 485                 490                 495
149 gga tta aca att aca gga gaa gat gct cct aac cta aaa aat atc gct    1536
150 Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala
151             500                 505                 510
153 ttt cat gaa gaa gat aac aat atg aac aac atc att ctg ttc gtg gga    1584
154 Phe His Glu Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly
155             515                 520                 525
157 act gat gca gct gac gtt att tac tta gat aac att aaa gta att gga    1632
158 Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly
159     530                 535                 540
161 aca gaa gtt gaa att cca gtt gtt cat gat cca aaa gga gaa gct gtt    1680
162 Thr Glu Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val
163 545                 550                 555                 560
165 ctt cct tct gtt ttt gaa gac ggt aca cgt caa ggt tgg gac tgg gct    1728
166 Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala
167             565                 570                 575
169 gga gag tct ggt gtg aaa aca gct tta aca att gaa gaa gca aac ggt    1776
170 Gly Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly
171             580                 585                 590
173 tct aac gcg tta tca tgg gaa ttt gga tat cca gaa gta aaa cct agt    1824
174 Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser
175             595                 600                 605
177 gat aac tgg gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg    1872
178 Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu
179     610                 615                 620
181 gtt cgc ggt gag aat gat tat gta gct ttt gat ttc tat cta gat cca    1920
182 Val Arg Gly Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro
183 625                 630                 635                 640
185 gtt cgt gca aca gaa ggc gca atg aat atc aat tta gta ttc cag cca    1968
186 Val Arg Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro
187             645                 650                 655
189 cct act aac ggg tat tgg gta caa gca cca aaa acg tat acg att aac    2016
190 Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn
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191           660            665            670
193 ttt gat gaa tta gag gaa gcg aat caa gta aat ggt tta tat cac tat   2064
194 Phe Asp Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr
195           675            680            685
197 gaa gtg aaa att aac gta aga gat att aca aac att caa gat gac acg   2112
198 Glu Val Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr
199     690            695            700
201 tta cta cgt aac atg atg atc att ttt gca gat gta gaa agt gac ttt   2160
202 Leu Leu Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe
203 705            710            715            720
205 gca ggg aga gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act   2208
206 Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr
207           725            730            735
209 act gag ccg gtt gaa cca gag cca gtt gat cct ggc gaa gag acg cca   2256
210 Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro
211          ·740            745            750
213 cct gtc gat gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa   2304
214 Pro Val Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys
215           755            760            765
217 gaa gag aaa gaa gag taa                                           2322
218 Glu Glu Lys Glu Glu
219     770
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222 <210> SEQ ID NO: 2
223 <211> LENGTH: 7.73
224 <212> TYPE: PRT
225 <213> ORGANISM: Bacillus sp.
227 <400> SEQUENCE: 2

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229 Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn
230 1               5                  10                 15
233 Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu
234            20                 25                 30
237 Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
238            35                 40                 45
241 Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
242     50                 55                 60
245 Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met
246 65                 70                 75                 80
249 Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro
250            85                 90                 95
253 Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu
254            100                105                110
257 Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
258            115                120                125
261 Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile
262     130                135                140
265 Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
266 145                150                155                160
269 Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
270            165                170                175
```

```
273 Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
274         180                 185                 190
277 Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
278         195                 200                 205
281 Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asn
282     210                 215                 220
285 Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
286 225                 230                 235                 240
289 Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
290                 245                 250                 255
293 Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
294         260                 265                 270
297 Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro
298         275                 280                 285
301 Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
302     290                 295                 300
305 Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
306 305                 310                 315                 320
309 Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp
310                 325                 330                 335
313 Pro Gly Pro Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly
314                 340                 345                 350
317 Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
318         355                 360                 365
321 Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
322     370                 375                 380
325 Gln Gly Phe Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala
326 385                 390                 395                 400
329 Val Asp Asn Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser
330                 405                 410                 415
333 Asn Asp Val Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala
334                 420                 425                 430
337 Asp Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr
338         435                 440                 445
341 Met Asp Val Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile
342     450                 455                 460
345 Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg
346 465                 470                 475                 480
349 Val Asn Ala Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala
350                 485                 490                 495
353 Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala
354                 500                 505                 510
357 Phe His Glu Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly
358         515                 520                 525
361 Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly
362     530                 535                 540
365 Thr Glu Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val
366 545                 550                 555                 560
369 Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/27/2005
PATENT APPLICATION: **US/10/538,343**   TIME: 14:48:13

Input Set : **A:\pto.kd.txt**
Output Set: **N:\CRF4\06272005\J538343.raw**

Invalid <213> Response:
**Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.**

Seq#:5,6,7,8,9,10,11,12

VERIFICATION SUMMARY
PATENT APPLICATION:　**US/10/538,343**

DATE: 06/27/2005
TIME: 14:48:13

Input Set : **A:\pto.kd.txt**
Output Set: **N:\CRF4\06272005\J538343.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date